

From: Chernyshev, Olga
Sent: Monday, March 28, 2005 3:28 PM
To: STIC-Biotech/ChemLib
Subject: 09/826,791 sequence search request

Please search SEQ ID NO: 2 in regular and pending databases. Please print out all the hits down to 95% identity.

Thank you very much!

Olga N. Chernyshev, Ph.D.

AU 1646

REM 3C89

2-0870

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Searcher: *Arnold*
Searcher Phone: 2- *2532*
Date Searcher Picked up: *4/1/05*
Date Completed: *4/14/05*
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: *2 (1x2)*
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

147517

STIC-Biotech/ChemLib

From: Chernyshev, Olga
Sent: Friday, March 11, 2005 9:23 AM
To: STIC-Biotech/ChemLib
Subject: 09/826,791: sequence search request

**Please search SEQ ID NOS: 1, 2, 5 and 6 in regular and pending databases.
Thank you very much!**

Olga N. Chernyshev, Ph.D.
AU 1646
REM 3C89
2-0870
mail 4C70

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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OM protein - protein search, using sw model

Run on: April 1, 2005, 11:58:33 / Search time 43 Seconds
(without alignments)
572,888 Million cell updates/sec

Title: US-09-826-791A-2

Perfect score: 1712
Sequence: 1 MERNGTFSNNNSRNCIENF.....KAKTKVFPVSVWLKRETRV 330

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 95%
Maximum Match 100%
Listing first 80 summaries

Database: Issued_Patents_AA:*

- 1: /cgn2_6/pcodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/pcodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/pcodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/pcodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/pcodata/1/1aa/ECTUS_COMB.pep:*
- 6: /cgn2_6/pcodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1703	99.5	346	4	US-09-585-876-2

ALIGNMENTS

RESULT 1
US-09-585-876-2
Sequence 2, Application US/09585876
Patent No. 6586205
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like molecule and
FILE REFERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585,876
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-585-876-2

Query Match 99.5%
Best Local Similarity 99.4%
Matches 328; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Score 1703; DB 4; Length 346;
Pred. No. 3.7e-124;
Search completed: April 1, 2005, 12:02:27
Job time: 43 secs

QY	1	MERNGTFSNNNSRNCIENF	KRPFPIVYLLIFPMQVVLGNGLSIYFLQPYKSTSVNVF	60
DB	17	MERNGTFSNNNSRNCIENF	KRPFPIVYLLIFPMQVVLGNGLSIYFLQPYKSTSVNVF	76
QY	61	MNLAIISDLFI	STLPFRADYLLRGSMIFGDLACRIMSISLVNMYSSIFPLTVASVVR	120
DB	77	MNLAIISDLFI	STLPFRADYLLRGSMIFGDLACRIMSISLVNMYSSIFPLTVASVVR	136
QY	121	FLAMVHPEFLHVT	SIRSAMILCGIIMLIMASSIMLDSGSEONGSVTSCLEMLYKIA	180
DB	137	FLAMVHPEFLHVT	SIRSAMILCGIIMLIMASSIMLDSGSEONGSVTSCLEMLYKIA	196
QY	181	KIOTMYIALVVGCL	LPFTLSICYLILIRVLLKVEVPSSGLRVSHRKALTITIIITLIIF	240
DB	197	KIOTMYIALVVGCL	LPFTLSICYLILIRVLLKVEVPSSGLRVSHRKALTITIIITLIIF	256
QY	241	FLCFLPYHTLRTVHL	LTWKVGLCKDRLHKALVITTLAANACFNPPLYYPAGENFQRL	300
DB	257	FLCFLPYHTLRTVHL	LTWKVGLCKDRLHKALVITTLAANACFNPPLYYPAGENFQRL	316
QY	301	KSALRKGHPOKAKTK	CVFPVSVWLKRETRV	330
DB	317	KSALRKGHPOKAKTK	CVFPVSVWLKRETRV	346